

SEQUENCE LISTING***SEQ ID 1 – NadA from strain 2996, with C-terminus deletion***

5 MKHFPSKVLTTAILATFCSGALAAATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAA
DVEADDFKGLGLKKVVTNLTKTVNENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGE
NITTFAEETKTNIVKIDKLEAVADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVK
AAETAAGKAEAAAGTANTAADKAEVAAKVTDIKADIATNKDNIAKKANSADVTTREESDSKFVRIDGLNATTE
KLDTRLASAEXSIADHDTRLNGLDKTVSDLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 2 – NadA from strain 2996, with C-terminus deletion and leader peptide processed

10 ATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDFKGLGLKKVVTNLTKTV
NENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAEETKTNIVKIDKLEAV
ADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAASETAAGKAEAAAGTANTAADKA
EVAIAAKVTDIKADIATNKDNIAKKANSADVTTREESDSKFVRIDGLNATTEKLDTRLASAEXSIADHDTRLNGL
DKTVSDLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 3 – ΔG741 from MC58 strain

15 VAADIGAGLADALTAPLDHDKGLQSLTLDQSVRKNEKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVSREFDFIRQ
IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLEGGGRATYRGT
AFGSDDAGGKLTYYTIDFAAKQNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEEKSYSGLIFGG
KAQEVAGSAEVTNNGIRHIGLAAKQ

SEQ ID 4 – 936 from MC58 strain with leader peptide processed

20 VSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYLQNNQTKGYTPQISVVGYNRHLHLLGQVATEG
EKQFVGQIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGIL
TPEEQAQITQKVSTTVGVQKVITLYQNYVQR

SEQ ID 5 – 953 from MC58 strain with leader peptide processed

25 ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDA
AQYPDIFRVSTKFNFNKGKLVSVGDLTMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYL
VNVGMTKSVRIDIQIEAAKQ

SEQ ID 6 – ΔG287 from MC58 strain

30 SPDVKSADTLSPAAPVSEKETEAKEDAPQAGSQGQAPSQAQSQDMAAVSEENTGNGGAVTADNPKNEDEVA
QNDMPQNAAGTDSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADMQDDPSAGGQAGNTAAQG
ANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDCSGNNFLDEEVQLKSEF
EKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRSARSRRSLPAEMPLIPVNQAD
TLIVDGEAVSLTGHSGNIFAPEGNRYLYTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRP
YPTRGRFAAKVDFGSKSVGDIIDSGDDLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSY
RPTDAEKGFGVFAGKKEQD

SEQ ID 7 – 287-953 hybrid

40 MASPDVKSADTLSPAAPVSEKETEAKEDAPQAGSQGQAPSQAQSQDMAAVSEENTGNGGAAATDKPKNEDE
GAQNDMPQNAADTDSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQDDPSAGGENAGNTAA
QGTNQAENNQTAGSQNPASSTNPATNSGGDFGRNTVGNSSVIDGPSQNTLTHCKGDCSGNNFLDEEVQLKS
EFEKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRSARSRRSLPAEMPLI
PVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYLYTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFH
TENGRPSPSRGRFAAKVDFGSKSVGDIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEV
AGKYSYRPTDAEKGFGVFAGKKEQDGSGGGGATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKR

DGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKGKLVSDGNLTMHGKTAPVKLKAEK
FNCYQSPMAKTEVCGGDFSTTIDRTKWGVLDLVNVGMTKSVRIDIQIEAAKQ*

SEQ ID 8 – 936-741 hybrid

5 MSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETTARSYL RQNNQTKGYTPQISVVGYNRHL LLLGQVATE
GEKQFVGQIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGI
LTPEEQAQITQKVSTTVGVQKVITLYQNYVQRGSGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN
EKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVS RFD FIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDS
EHSGKMVAKRQFRIGDIAGEHTSF DKLPEGGRATYRGTAFGSDDAGGKLT YTIDFAAKQNGKIEHLKSPELNV
DLAAADIKPDGKRHAVISGSVLYNQA EKG SYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLA AKQ*

10 ***SEQ ID 9 – linker***

GSGGGG

SEQ ID 10 – 741 sequence

15 CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN EKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVS
RFD FIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSF DKLPEGG
RATYRGTAFGSDDAGGKLT YTIDFAAKQNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQA EKG SY
SLGIFGGKAQEVAGSAEVKTVNGIRHIGLA AKQ

SEQ ID 11 – 741 sequence

20 CSSGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKN EKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVS
RFD FIRQIEVDGQLITLESGEFQIYKQDHS AVVALQIEKINNPDKIDSLINQRSFLV SGLGGEHTAFNQLPDGK
AEYHGKAFSSDDAGGKLT YTIDFAAKQGHGKIEHLKTP EQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYH
LALFGDRAQEIAGSATVKIG EKVHEIGIAGKQ

SEQ ID 12 – 741 sequence

25 CSSGGGGSGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLED SIPQNGTLTLSAQGA EKT FKAGDKDNSLNTG
KLKNDKISRFDVQKIEVDGQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTD SLINQRSFLV SGLGGEHTA
FNQLPGGKA EYHGKAFSSDDPNGR LHYSIDFTKKQGYGRIEHLK TLEQNVELAAAELKADEKSHAVILGDTRYG
SEEKGTYHLALFGDRAQEIAGSATVKIG EKVHEIGIAGKQ